

0400 03-08-01

#2

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/776,865

DATE: 03/02/2001
 TIME: 13:48:32

Input Set : A:\Sequence.txt
 Output Set: N:\CRF3\03022001\I776865.raw

ENTERED

3 <110> APPLICANT: Hellerqvist, Carl
 5 <120> TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
 7 <130> FILE REFERENCE: 22100-0100 46126-252687
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/776,865
 C--> 9 <141> CURRENT FILING DATE: 2001-02-02
 9 <150> PRIOR APPLICATION NUMBER: US 60/179,870
 10 <151> PRIOR FILING DATE: 2000-02-02
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2930
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (263)..(1870)
 25 <400> SEQUENCE: 1

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30	gcgggagacg gtcgtccgaa caccggctcc cggcatgcg tagaccggcg ggcggagcgg	180
32	gtcactttg cgccaatcct acgagaactc ccagaactcc gcttcctag tccaacccaa	240
34	gccagagtgt cccacacctt ag atg gcg gcg ggg gcg atg aca ccg ccc cgc	292
35	Met Ala Ala Gly Ala Met Thr Pro Pro Arg	
36	1 5 10	
38	ccg gtc cag cca gct cgg ccc ggg ggc ttc ggg ctg tcg ggc cgg cgc	340
39	Pro Val Gln Pro Ala Arg Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg	
40	15 20 25	
42	tcc ctt ctc tgc cag gtg gcg agt aca cct gct cac gta ggc gtc atg	388
43	Ser Leu Leu Cys Gln Val Ala Ser Thr Pro Ala His Val Gly Val Met	
44	30 35 40	
46	agg tct ccg gtt cga gac ctg gcc cgg aac gat ggc gag gag agc acg	436
47	Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr	
48	45 50 55	
50	gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct cca	484
51	Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro	
52	60 65 70	
54	gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt ggt	532
55	Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly	
56	75 80 85 90	
58	ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta gtg	580
59	Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu Val	
60	95 100 105	
62	gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc aag	628
63	Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys	
64	110 115 120	
66	gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa acg	676
67	Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln Thr	

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68	125	130	135	
70	ggt aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc ggt	724		
71	Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly			
72	140 145 150			
74	tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat gtt	772		
75	Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val			
76	155 160 165 170			
78	gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt ggc	820		
79	Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu Gly			
80	175 180 185			
82	act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga gtt	868		
83	Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly Val			
84	190 195 200			
86	gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt gtt	916		
87	Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly Val			
88	205 210 215			
90	aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct ctt	964		
91	Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro Leu			
92	220 225 230			
94	gaa aga agc aaa ctt ctt agc att tcg tat gca gga gca cag ctt ggg	1012		
95	Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly			
96	235 240 245 250			
98	aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg aat	1060		
99	Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn			
100	255 260 265			
102	tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg ttt	1108		
103	Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe			
104	270 275 280			
106	ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag aga	1156		
107	Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys Arg			
108	285 290 295			
110	att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat cag	1204		
111	Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln			
112	300 305 310			
114	ctt tct tca cag aag tca gtg cgg tgg gta ccc att tta aaa tcc ctg	1252		
115	Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser Leu			
116	315 320 325 330			
118	cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act ttt	1300		
119	Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr Phe			
120	335 340 345			
122	tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta agg	1348		
123	Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg			
124	350 355 360			
126	ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta ggc	1396		
127	Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly			
128	365 370 375			
130	tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta agg	1444		
131	Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg			
132	380 385 390			

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134 gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc ctt      1492
135 Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser Leu
136 395                               400                               405                               410
138 ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc att      1540
139 Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile
140                               415                               420                               425
142 ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca aca      1588
143 Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr
144                               430                               435                               440
146 ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat att      1636
147 Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile
148                               445                               450                               455
150 gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc      1684
151 Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala
152                               460                               465                               470
154 act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct      1732
155 Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro
156 475                               480                               485                               490
158 gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct      1780
159 Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala
160                               495                               500                               505
162 att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa      1828
163 Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu
164                               510                               515                               520
166 gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac      1870
167 Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
168                               525                               530                               535
170 tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttatttata atgtaacctc      1930
172 aaagtgcctt ctgtatttgt taagcattct atgtcttttt ttaattgtac ttgtattaga      1990
174 tttttaaggc ctataatcat gaaatatcac tagttgccag aataataaaa tgaactgtgt      2050
176 ttaattatga ataatatgta agctaggact totacttttag gttcacatac ctgcctgcta      2110
178 gtcgggcaac atgaagtagg acagttctgt tgatttttta gggccatact aaagggaatg      2170
180 agctgaaaca gacctcctga taccttttget taattaaact agatgataat tctcaggtag      2230
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184 agacctcaaa ctttagcatc tctgtggagc tgccatccac tgtataattt cgctggcaa      2350
186 ctggactgag gggagtgtgc ccaggcagct gccagcact ccctccctgg cttcagggtc      2410
188 agagtgccca gcgtttatca gaggcagcat ccaagcccag agccagtgtc gactcttcgg      2470
190 ctggtgcctt tctctgagg ggctatcaat gtgtagataa agccctgagt aggcaagagc      2530
192 agtgagatcc actgctatgg tcttgataca tctcaaaact ttcccttccc agcacagagg      2590
194 aatattggct ggcattgaac ctgcaaaaaga aaaatgcgaa gcggccgggc acggtggctc      2650
196 atgcctgtaa toccagcact ttggggggct gaggtgggcy aatcatgaga tcaggagttc      2710
198 gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaattagct      2770
200 gggcgtgggt acgggcgcct gtaatccag atactcagga ggctgaggta ggagaatcac      2830
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207 <210> SEQ ID NO: 2
208 <211> LENGTH: 536
209 <212> TYPE: PRT
210 <213> ORGANISM: Homo sapiens

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212 <400> SEQUENCE: 2

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214 Met Ala Ala Gly Ala Met Thr Pro Pro Arg Pro Val Gln Pro Ala Arg
215 1 5 10 15
218 Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg Ser Leu Leu Cys Gln Val
219 20 25 30
222 Ala Ser Thr Pro Ala His Val Gly Val Met Arg Ser Pro Val Arg Asp
223 35 40 45
226 Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr Asp Arg Thr Pro Leu Leu
227 50 55 60
230 Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro Val Cys Cys Ser Ala Arg
231 65 70 75 80
234 Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly Phe Phe Ile Val Tyr Ala
235 85 90 95
238 Leu Arg Val Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn
239 100 105 110
242 Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys Ala Cys Pro Glu His Ser
243 115 120 125
246 Ala Pro Ile Lys Val His His Asn Gln Thr Gly Lys Lys Tyr Gln Trp
247 130 135 140
250 Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr
251 145 150 155 160
254 Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val Ala Ser Lys Ile Gly Gly
255 165 170 175
258 Lys Met Leu Leu Gly Phe Gly Ile Leu Gly Thr Ala Val Leu Thr Leu
259 180 185 190
262 Phe Thr Pro Ile Ala Ala Asp Leu Gly Val Gly Pro Leu Ile Val Leu
263 195 200 205
266 Arg Ala Leu Glu Gly Leu Gly Glu Gly Val Thr Phe Pro Ala Met His
267 210 215 220
270 Ala Met Trp Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu
271 225 230 235 240
274 Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly Thr Val Ile Ser Leu Pro
275 245 250 255
278 Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr
279 260 265 270
282 Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe Leu Leu Trp Ile Trp Leu
283 275 280 285
286 Val Ser Asp Thr Pro Gln Lys His Lys Arg Ile Ser His Tyr Glu Lys
287 290 295 300
290 Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln Leu Ser Ser Gln Lys Ser
291 305 310 315 320
294 Val Pro Trp Val Pro Ile Leu Lys Ser Leu Pro Leu Trp Ala Ile Val
295 325 330 335
298 Val Ala His Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu
299 340 345 350
302 Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg Phe Asn Val Gln Glu Asn
303 355 360 365
306 Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly Ser Trp Leu Cys Met Ile
307 370 375 380

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310 Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg Ala Lys Trp Asn Phe Ser
311 385                      390                      395                      400
314 Thr Leu Cys Val Arg Arg Ile Phe Ser Leu Ile Gly Met Ile Gly Pro
315                      405                      410                      415
318 Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu
319                      420                      425                      430
322 Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly Gly Phe Cys Ser
323                      435                      440                      445
326 Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly
327                      450                      455                      460
330 Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Val
331 465                      470                      475                      480
334 Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn Thr Val Gly Glu
335                      485                      490                      495
338 Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn Val Phe Gly Ala
339                      500                      505                      510
342 Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Leu
343                      515                      520                      525
346 Asn Asp His His Gly His Arg His
347                      530                      535
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351 <211> LENGTH: 2844
352 <212> TYPE: DNA
353 <213> ORGANISM: Ovis sp.
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
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359 <400> SEQUENCE: 3
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363                      Met Lys Ser Pro Val Ser Asp Leu Ala Pro
364                      1                      5                      10
366 agc gac ggc gag gag ggc tcg gac cgc aca ccg ctc ctg cag cgc gcc      161
367 Ser Asp Gly Glu Glu Gly Ser Asp Arg Thr Pro Leu Leu Gln Arg Ala
368                      15                      20                      25
370 ccg cgg gcg gaa ccc gct cca gta tgc tgc tct gct cgt tac aac cta      209
371 Pro Arg Ala Glu Pro Ala Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu
372                      30                      35                      40
374 gca ttt ttg tcc ttt ttt ggt ttc ttc gtt ctc tat tca tta cgg gtg      257
375 Ala Phe Leu Ser Phe Phe Gly Phe Phe Val Leu Tyr Ser Leu Arg Val
376                      45                      50                      55
378 aat ctg agc gtt gca cta gtg gac atg gtg gat tca aac aca act gcc      305
379 Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn Thr Thr Ala
380                      60                      65                      70
382 aaa gat aat aga acg tcc tac gag tgt gca gag cat tct gct ccc ata      353
383 Lys Asp Asn Arg Thr Ser Tyr Glu Cys Ala Glu His Ser Ala Pro Ile
384 75                      80                      85                      90
386 aaa gtt ctt cac aac caa acg ggt aaa aag tac cgg tgg gat gca gaa      401
387 Lys Val Leu His Asn Gln Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu

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Input Set : A:\Sequence.txt
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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date